

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/940,063

DATE: 11/13/2001

TIME: 15:11:42

Input Set : N:\Crif3\RULE60\09940063.txt

Output Set: N:\CRF3\11132001\I940063.raw

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4 <110> APPLICANT: Briskin, Michael J.
5     Murphy, Kristine E.
6     Wilbanks, Alyson M.
7     Wu, Lijun
9 <120> TITLE OF INVENTION: Novel Antibodies and Ligands for "Bonzo"
10    Chemokine Receptor
12 <130> FILE REFERENCE: 1855.1070000
14 <140> CURRENT APPLICATION NUMBER: 09/940,063
15 <141> CURRENT FILING DATE: 2001-08-27
17 <150> PRIOR APPLICATION NUMBER: 09/449,437
18 <151> PRIOR FILING DATE: 1999-11-24
20 <160> NUMBER OF SEQ ID NOS: 18
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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25 <211> LENGTH: 1029
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
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32 gtgtttgtct gtggtctggt ggggaactct ctggtgctgg tcatatccat cttctacccat      180
33 aagttgcaga gcctgacgga tgtgttcctg gtgaacctac ccctggctga cctggtgttt      240
34 gtctgcactc tgcccttctg ggcctatgca ggcattccat aatgggtgtt tggccaggctc      300
35 atgtgcaaga gcctactggg catctacact attaacttct acacgtccat gctcatcctc      360
36 acctgcatca ctgtggatcg ttctattgta gtggttaagg ccaccaaggc ctacaaccag      420
37 caagccaaga ggatgacctg gggcaaggct accagcttgc tcatctgggt gatatccctg      480
38 ctggtttcct tgccccaat tatctatggc aatgtcttta atctcgacaa gctcatatgt      540
39 ggttaccatg acgaggcaat ttccactgtg gttcttgcca ccagatgac actggggttc      600
40 ttcttgccac tgctcaccat gattgtctgc tattcagtc taatcaaac actgcttcat      660
41 gctggaggct tccagaagca cagatctcta aagatcatct tctggtgat ggctgtgttc      720
42 ctgctgaccc agatgccctt caacctcatg aagttcatcc gcagcacaca ctgggaatac      780
43 tatgccatga ccagctttca ctacaccatc atggtgacag aggccatcgc atacctgagg      840
44 gcctgcctta accctgtgct ctatgccttt gtcagcctga agtttcgaaa gaacttctgg      900
45 aaacttgtga aggacattgg ttgcctccct taccttgggg tctcacatca atggaaatct      960
46 tctgaggaca attccaagac tttttctgcc tcccacaatg tggaggccac cagcatgttc      1020
47 cagttatag                                     1029
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50 <211> LENGTH: 342
51 <212> TYPE: PRT
52 <213> ORGANISM: Homo Sapiens
54 <400> SEQUENCE: 2
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56 1           5           10           15
57 Asp Ser Ser Gln Glu Glu His Gln Asp Phe Leu Gln Phe Ser Lys Val
58           20           25           30
59 Phe Leu Pro Cys Met Tyr Leu Val Val Phe Val Cys Gly Leu Val Gly
60           35           40           45

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61 Asn Ser Leu Val Leu Val Ile Ser Ile Phe Tyr His Lys Leu Gln Ser
62      50                      55                      60
63 Leu Thr Asp Val Phe Leu Val Asn Leu Pro Leu Ala Asp Leu Val Phe
64 65      70                      75                      80
65 Val Cys Thr Leu Pro Phe Trp Ala Tyr Ala Gly Ile His Glu Trp Val
66      85                      90                      95
67 Phe Gly Gln Val Met Cys Lys Ser Leu Leu Gly Ile Tyr Thr Ile Asn
68      100                     105                     110
69 Phe Tyr Thr Ser Met Leu Ile Leu Thr Cys Ile Thr Val Asp Arg Phe
70      115                     120                     125
71 Ile Val Val Val Lys Ala Thr Lys Ala Tyr Asn Gln Gln Ala Lys Arg
72      130                     135                     140
73 Met Thr Trp Gly Lys Val Thr Ser Leu Leu Ile Trp Val Ile Ser Leu
74 145      150                     155                     160
75 Leu Val Ser Leu Pro Gln Ile Ile Tyr Gly Asn Val Phe Asn Leu Asp
76      165                     170                     175
77 Lys Leu Ile Cys Gly Tyr His Asp Glu Ala Ile Ser Thr Val Val Leu
78      180                     185                     190
79 Ala Thr Gln Met Thr Leu Gly Phe Phe Leu Pro Leu Leu Thr Met Ile
80      195                     200                     205
81 Val Cys Tyr Ser Val Ile Ile Lys Thr Leu Leu His Ala Gly Gly Phe
82      210                     215                     220
83 Gln Lys His Arg Ser Leu Lys Ile Ile Phe Leu Val Met Ala Val Phe
84 225      230                     235                     240
85 Leu Leu Thr Gln Met Pro Phe Asn Leu Met Lys Phe Ile Arg Ser Thr
86      245                     250                     255
87 His Trp Glu Tyr Tyr Ala Met Thr Ser Phe His Tyr Thr Ile Met Val
88      260                     265                     270
89 Thr Glu Ala Ile Ala Tyr Leu Arg Ala Cys Leu Asn Pro Val Leu Tyr
90      275                     280                     285
91 Ala Phe Val Ser Leu Lys Phe Arg Lys Asn Phe Trp Lys Leu Val Lys
92      290                     295                     300
93 Asp Ile Gly Cys Leu Pro Tyr Leu Gly Val Ser His Gln Trp Lys Ser
94 305      310                     315                     320
95 Ser Glu Asp Asn Ser Lys Thr Phe Ser Ala Ser His Asn Val Glu Ala
96      325                     330                     335
97 Thr Ser Met Phe Gln Leu
98      340
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101 <211> LENGTH: 1763
102 <212> TYPE: DNA
103 <213> ORGANISM: Homo sapiens
105 <400> SEQUENCE: 3
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107 ttctgtcctt gctgggtgtac ctgactcagc caggcaatgg caacgagggc agcgtcactg      120
108 gaagttgtta ttgtggtaaa agaatttctt ccgactcccc gccatcggtt cagttcatga      180
109 atcgcttccg gaaacacctg agagcttacc atcggtgtct atactacacg aggttccagc      240
110 tcctttcctg gagcgtgtgt ggaggcaaca aggacccatg gggttcaggaa ttgatgagct      300
111 gtcttgatct caaagaatgt ggacatgctt actcgggggat tgtggcccac cagaagcatt      360

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112 tacttcctac cagcccccca atttctcagg cctcagaggg ggcattcttca gatatccaca 420
113 cccctgccca gatgctcctg tccaccttgc agtccactca gcgccccacc ctcccagtag 480
114 gatcactgtc ctcggaacaa gagctcactc gtcccaatga aaccaccatt cacactgcgg 540
115 gccacagtct ggcagttggg cctgaggctg gggagaacca gaagcagccg gaaaaaaaaatg 600
116 ctggtcccac agccaggaca tcagccacag tgccggtcct gtgcctcctg gccatcatct 660
117 tcctcctcac cgcagccctt tcctatgtgc tgtgcaagag gaggaggggg cagtcaccgc 720
118 agtccctctc agatctgccg gttcattata tacctgtggc acctgactct aataacctgag 780
119 ccaagaatgg aagcttgtga ggagacggac tctatgttgc ccaggctgtt atggaactcc 840
120 tgagtcaagt gatccctcca ccttggcctc tgaagggtgc aggattatag gcgtcaccta 900
121 ccacatccag cctacacgta tttgttaata tctaaccatg gactaaccag ccactgccct 960
122 ctcttagggc cctcatTTaa aaacggttat actataaaat ctgcttttca cactgggtga 1020
123 taataacttg gacaaattct atgtgtatTT tgttttgttt tgctttgctt tgttttgaga 1080
124 cggagtctcg ctctgtcatc caggctggag tgcagtggca tgatctcggc tcaactgaac 1140
125 ccccatctcc caggttcaag cgattctcct gcctcctcct gagtagctgg gactacaggT 1200
126 gctcaccacc acaccggct aattttttgt atttttagta gagaccgggg tttcaccatg 1260
127 ttgaccaggc tggctctgaa ctctgacct ggtgatctgc ccaccaggc ctcccaaagt 1320
128 gctgggatta aagggtgtgag ccacatgcc tggccctatg tgtgtttttt aactactaaa 1380
129 aattattttt gtaatgattg agtcttcttt atggaaacaa ctggcctcag cccttgcgcc 1440
130 ctactgtga ttcttggtt ctttttttgc tgatgggtcc ccctcgccc aaatctctct 1500
131 cccagtacac cagttgttcc tccccacct cagccctctc ctgcatcctc ctgtaccgc 1560
132 aacgaaggcc tgggttttcc caccctccct ccttagcagg tgccgtgctg ggacaccata 1620
133 cgggttggtt tcacctctc agtcccttgc ctaccccagt gagagtctga tcttgTTTT 1680
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139 <212> TYPE: PRT
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142 <400> SEQUENCE: 4
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146 20 25 30
147 Ser Val Thr Gly Ser Cys Tyr Cys Gly Lys Arg Ile Ser Ser Asp Ser
148 35 40 45
149 Pro Pro Ser Val Gln Phe Met Asn Arg Leu Arg Lys His Leu Arg Ala
150 50 55 60
151 Tyr His Arg Cys Leu Tyr Tyr Thr Arg Phe Gln Leu Leu Ser Trp Ser
152 65 70 75 80
153 Val Cys Gly Gly Asn Lys Asp Pro Trp Val Gln Glu Leu Met Ser Cys
154 85 90 95
155 Leu Asp Leu Lys Glu Cys Glu His Ala Tyr Ser Gly Ile Val Ala His
156 100 105 110
157 Gln Lys His Leu Leu Pro Thr Ser Pro Pro Thr Ser Gln Ala Ser Glu
158 115 120 125
159 Gly Ala Ser Ser Asp Ile His Thr Pro Ala Gln Met Leu Leu Ser Thr
160 130 135 140
161 Leu Gln Ser Thr Gln Arg Pro Thr Leu Pro Val Gly Ser Leu Ser Ser
162 145 150 155 160

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163 Asp Lys Glu Leu Thr Arg Pro Asn Glu Thr Thr Ile His Thr Ala Gly
164                               165                               170                               175
165 His Ser Leu Ala Val Gly Pro Glu Ala Gly Glu Asn Gln Lys Gln Pro
166                               180                               185                               190
167 Glu Lys Asn Ala Gly Pro Thr Ala Arg Thr Ser Ala Thr Val Pro Val
168                               195                               200                               205
169 Leu Cys Leu Leu Ala Ile Ile Phe Ile Leu Thr Ala Ala Pro Ser Tyr
170                               210                               215                               220
171 Val Leu Cys Lys Arg Arg Gly Gln Ser Pro Gln Ser Ser Pro Asp
172 225                               230                               235                               240
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174                               245                               250
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183 gcccggatcg gggaagtga agtgcctcgg aggaggagg ccggtccggc agtgcagccg      120
184 cctcacaggt cggcggacgg gccaggcggg cggcctcctg aaccgaaccg aatcggctcc      180
185 tcgggcccgtc gtccctccgc ccctcctcgc ccgcccggc agttttcttt cggtttcttc      240
186 caagattcct ggccttccct cgacggagcc gggcccagtg cgggggcgca gggcgcggga      300
187 gctccacctc ctcggttttc cctgcgtcca gaggtggca tggcgcgggc cgagtactga      360
188 gcgcacggtc ggggcacagc agggccggtg ggtgcagctg gctcgcgcct cctctccggc      420
189 cgccgtctcc tccggtcccc ggcgaaagcc attgagacac cagctggacg tcacgcgccg      480
190 gagcatgtct gggagtcaga gcgaggtggc tccatccccg cagagtccgc ggagccccga      540
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192 ggtgtacctg actcagccag gcaatggcaa cgagggcagc gtcaactgaa gttgttattg      660
193 tggtaaaaga atttcttccg actccccgcc atcgtttcag ttcatgaatc gtctccggaa      720
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195 cgtgtgtgga ggcaacaagg acccatgggt tcaggaattg atgagctgtc ttgatctcaa      840
196 agaattgtga catgcttact cggggattgt ggcccaccag aagcatttac ttctaccag      900
197 ccccccaact tctcaggcct cagagggggc atcttcagat atccacaccc ctgccagat      960
198 gctcctgtcc accttgcaat ccactcagcg ccccccctc ccagtaggat cactgtcttc      1020
199 ggacaaagag ctcaactcgt ccaatgaaac caccattcac actgcggggc acagtctggc      1080
200 agttgggcct gaggtctggg agaaccagaa gcagccggaa aaaaatgctg gtcccacagc      1140
201 caggacatca gccacagtgc cgtcctgtg cctcctggcc atcatcttca tcctcaccgc      1200
202 agccctttcc tatgtgctgt gcaagaggag gagggggcag tcaccgcagt cctctccaga      1260
203 tctgccggtt cattatatac ctgtggcacc tgactctaata acctgagcca agaattggaag      1320
204 cttgtgagga gacggactct atgttgccca ggctgttatg gaactcctga gtcaagtgat      1380
205 cctcccacct tggcctctga aggtgcgagg attataggcg tcacctacca catccagcct      1440
206 acacgtattt gttaatatct aacataggac taaccagcca ctgccctctc ttaggccccct      1500
207 catttaaaaa cggttatact ataaaaatctg cttttcacac tgggtgataa taacttgga      1560
208 aaattctatg tgtattttgt tttgttttgc tttgctttgt tttgagacgg agtctcgtc      1620
209 tgtcatccag gctggagtgc agtggcatga tctcggctca ctgcaacccc catctccag      1680
210 gttcaagcga ttctcctgcc tcctcctaag tagctgggac tacagggtgt caccaccaca      1740
211 cccggctaata tttttgtatt tttagttag acgggggttc accatgttga ccaggctgg      1800
212 ctcgaactcc tgacctgggt atctgcccac ccaggcctcc caaagtgtg ggattaaagg      1860
213 tgtgagccac catgcctggc cctatgtgtg ttttttaact actaaaaatt aattttttgta      1920

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214 tgattgagtc ttctttatgg aaacaactgg cctcagccct tgcgccctta ctgtgattcc 1980
215 tggcttcatt ttttgctgat ggttccccct cgtcccaaat ctctctccca gtacaccagt 2040
216 tgttcctccc ccacctcagc cctctcctgc atcctcctgt acccgcaacg aaggcctggg 2100
217 ctttcccacc ctccctcctt agcagggtgcc gtgctgggac accatacggg ttggtttcac 2160
218 ctcctcagtc ccttgccctac cccagtggag gtctgatctt gtttttattg ttattgcttt 2220
219 tattattatt gcttttatta tcattaaaaa tctagttctt gttttgtctc tcaaaaaaaaa 2280
220 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2309

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223 &lt;211&gt; LENGTH: 254

224 &lt;212&gt; TYPE: PRT

225 &lt;213&gt; ORGANISM: Homo sapiens

227 &lt;400&gt; SEQUENCE: 6

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231 20 25 30
232 Ser Val Thr Gly Ser Cys Tyr Cys Gly Lys Arg Ile Ser Ser Asp Ser
233 35 40 45
234 Pro Pro Ser Val Gln Phe Met Asn Arg Leu Arg Lys His Leu Arg Ala
235 50 55 60
236 Tyr His Arg Cys Leu Tyr Tyr Thr Arg Phe Gln Leu Leu Ser Trp Ser
237 65 70 75 80
238 Val Cys Gly Gly Asn Lys Asp Pro Trp Val Gln Glu Leu Met Ser Cys
239 85 90 95
240 Leu Asp Leu Lys Glu Cys Gly His Ala Tyr Ser Gly Ile Val Ala His
241 100 105 110
242 Gln Lys His Leu Leu Pro Thr Ser Pro Pro Thr Ser Gln Ala Ser Glu
243 115 120 125
244 Gly Ala Ser Ser Asp Ile His Thr Pro Ala Gln Met Leu Leu Ser Thr
245 130 135 140
246 Leu Gln Ser Thr Gln Arg Pro Thr Leu Pro Val Gly Ser Leu Ser Ser
247 145 150 155 160
248 Asp Lys Glu Leu Thr Arg Pro Asn Glu Thr Thr Ile His Thr Ala Gly
249 165 170 175
250 His Ser Leu Ala Val Gly Pro Glu Ala Gly Glu Asn Gln Lys Gln Pro
251 180 185 190
252 Glu Lys Asn Ala Gly Pro Thr Ala Arg Thr Ser Ala Thr Val Pro Val
253 195 200 205
254 Leu Cys Leu Leu Ala Ile Ile Phe Ile Leu Thr Ala Ala Leu Ser Tyr
255 210 215 220
256 Val Leu Cys Lys Arg Arg Arg Gly Gln Ser Pro Gln Ser Ser Pro Asp
257 225 230 235 240
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261 &lt;210&gt; SEQ ID NO: 7

262 &lt;211&gt; LENGTH: 439

263 &lt;212&gt; TYPE: DNA

264 &lt;213&gt; ORGANISM: Homo sapiens

266 &lt;400&gt; SEQUENCE: 7

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/940,063

DATE: 11/13/2001

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